

Access DB# 164534

CRFE

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 8/31/05
Art Unit: 1636 Phone Number 30272-0767 Serial Number: 10/643627
Mail Box and Bldg/Room Location: Room 2A79 Results Format Preferred (circle): PAPER DISK E-MAIL
Mailbox: 2C70

If more than one search is submitted, please prioritize searches in order of need.

mej

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

*I'd like search for fragments of SEQ ID NO: 4
or SEQ ID NO: 6 at least 10 consecutive amino
acids in length or at least 40 consecutive
amino acids in length.*

4 aa 398

6 aa 398

Thanks

mej

*9/16/05
JH*

STAFF USE ONLY

Searcher: Beverly 2528

Type of Search _____

NA Sequence (#) _____

Vendors and cost where applicable _____

STN _____

OFFICIAL USE ONLY

165100

ACCESS DB #

PLEASE PRINT CLEARLY

10

Scientific and Technical Information Center

SEARCH REQUEST FORM

CRFB

Requester's Full Name: DAVID GURZO Examiner #: 70677 Date: 9/8/05
Art Unit: 1636 Phone Number: 2-0767 Serial Number: 10/643627
Location (Bldg/Room#): Rm 2A79 (Mailbox #): 2C70 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Date: _____

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search for fragments of SEQ ID NO: 63
at least 10 consecutive amino acids in length or
at least 20 consecutive amino acids in length or at
least 40 consecutive amino acids in length.

63-397 A1A

Complete
9/15/05
J.H.

T. Banks

RECEIVED
SEP - 8 2005
TECH/CHEM. DIVISION
(STIC)

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OM protein - protein search, using sw model

Run on: September 15, 2005, 09:01:04 ; Search time 170 Seconds
(without alignments)
903.199 Million cell updates/sec

Title: US-10-643-627-63

Perfect score: 397
Sequence: 1 MRSPSAAMLGAAIILAAASL.....KHSRKSSTSSSTTVKTSY 397

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size: 40

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_1Dec04:
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 296 | 74.6 | 397 | 2 | AAR6923 Human C14 |
| 2 | 296 | 74.6 | 397 | 2 | AAW01955 Human C14 |
| 3 | 114 | 28.7 | 394 | 2 | AAW51408 Human pro |
| 4 | 114 | 28.7 | 397 | 3 | AAW55641 Human PAR |
| 5 | 114 | 28.7 | 397 | 5 | AAE26678 Human coa |
| 6 | 114 | 28.7 | 397 | 6 | ABG73508 Human par |
| 7 | 114 | 28.7 | 397 | 7 | ABG73508 Human par |
| 8 | 114 | 28.7 | 397 | 8 | AD62812 Human pro |
| 9 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 10 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 11 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 12 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 13 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 14 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 15 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 16 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 17 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 18 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 19 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |
| 20 | 114 | 28.7 | 397 | 8 | AD61221 Human coa |

ALIGNMENTS

RESULT 1

AAR6923 standard; protein; 397 AA.

AC AAR6923;

DT 25-MAR-2003 (reviewed)

DT 22-AUG-1995 (first entry)

DE Human C140 receptor encoded by cDNA.

DE G-protein-coupled receptor; G-protein; C140 receptor.

OS Homo sapiens.

PN WO9503318-A1.

PD 02-FEB-1995.

PF 26-JUL-1994; 94WO-US008536.

PR 26-JUL-1993; 93US-00097938.

PA (COR-) COR THERAPEUTICS.

PI Scarborough RM, Sundelin J;

DR WPI; 1995-075182/10.

DR N-Psdb; AA084560.

PT New DNA encoding recombinant C140 receptor - and novel agonists and antagonists and specific antibodies with therapeutic and diagnostic applications.

PS Example; Fig 11; 57pp; English.

CC A human intestinal tumor cDNA library was subjected to PCR using primers designed from the genomic clone (see AA084558) and the amplified fragment was cloned in pSOS and sequenced. There are four AA differences between the cDNA encoded sequence and that encoded by the genomic DNA. The CC genomic DNA sequence and deduced AA sequence are given in AA084560 & AA084561. (Updated on 25-MAR-2003 to correct PN field.)

CC AAR6923. (Updated on 25-MAR-2003 to correct PN field.)

CC Sequence 397 AA;

Query Match 74.6%; Score 296; DB 2; Length 397;

Best Local Similarity 99.7%; Pred. No. 2.9e-276;

Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MRSPSAAMLGAAIILAAASLSCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETFS | 60 |
| DB | 1 | MRSPSAAMLGAAIILAAASLSCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETFS | 60 |
| QY | 61 | VDEPFAVYAGLTVPLPIVYTVFAVGLPENGMAVFLPRTKKGPAVIYMANLALA | 120 |
| DB | 61 | VDEPFAVYAGLTVPLPIVYTVFAVGLPENGMAVFLPRTKKGPAVIYMANLALA | 120 |
| QY | 121 | DLLSVIWPFLKLAHYHGNMVIYGEALCNVLIQFYGNMYSILEPNTCLSVORVYVNP | 180 |
| DB | 121 | DLLSVIWPFLKLAHYHGNMVIYGEALCNVLIQFYGNMYSILEPNTCLSVORVYVNP | 180 |
| QY | 181 | MGRSRKANIAGISLAIWLTPLVYVYKQTFIPALNITTCCHDVLPEQLVGDWF | 240 |
| DB | 181 | MGRSRKANIAGISLAIWLTPLVYVYKQTFIPALNITTCCHDVLPEQLVGDWF | 240 |
| QY | 241 | NYFLSLAIGVFLPFAVLTASAVYLMIRMSAMDENSKRRRAIKLIVTVLGVYLCF | 300 |
| DB | 241 | NYFLSLAIGVFLPFAVLTASAVYLMIRMSAMDENSKRRRAIKLIVTVLGVYLCF | 300 |
| QY | 301 | TPSNLLLVVHYFLIKSGQSHVYALYIVALCLSTLNSCIDPFRVYVSHDFDHAKNAL | 360 |
| DB | 301 | TPSNLLLVVHYFLIKSGQSHVYALYIVALCLSTLNSCIDPFRVYVSHDFDHAKNAL | 360 |

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OM protein - protein search, using sw model

Run on: September 15, 2005, 09:14:51 ; Search time 41 Seconds

(without alignments)
931.660 Million cell updates/sec

Title: US-10-643-627-63

Perfect score: 397
Sequence: 1 MRSPSAAMLGAILLAASL.....KHSRKSSVSSSTVTYKTSY 397

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 9621673 residues

Word size : 10

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : PIR 79:*

1: pir1:*\n2: pir2:*\n3: pir3:*\n4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 114 | 28.7 | 397 | 2 S66518 | proteinase-activat |
| 2 | 34 | 8.6 | 399 | 2 148705 | proteinase activat |
| 3 | 10 | 2.5 | 425 | 2 A37912 | thrombin receptor |
| 4 | 10 | 2.5 | 427 | 2 S17148 | alpha-thrombin rec |
| 5 | 10 | 2.5 | 432 | 2 A43448 | thrombin receptor |

ALIGNMENTS

RESULT 1
S66518
proteinase-activated receptor 2 precursor - human
C/Species: Homo sapiens (man)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66518; S64709; G02131
R/Nystedt, S.; Emlason, K.; Larsen, A.K.; Strombeck, B.; Sundelin, J.
Eur. J. Biochem. 232, 84-89, 1995
A/Title: Molecular cloning and functional expression of the gene encoding the human prot
A/Reference number: S66518; MUID:96048032; PMID:7556175
A/Accession: S66518
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-397 <NTS>
A/Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:g106084; PID:CAA90290.1; PID:g100
R/Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn
Biochem. J. 314, 1009-1016, 1996
A/Title: Molecular cloning, expression and potential functions of the human proteinase-
A/Reference number: S64709; MUID:96177879; PMID:8615752

A/Accession: S64709
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-137, 'A', 139-397 <BOE>
A/Cross-references: EMBL:U34038; NID:g1041728; PID:ABA47871.1; PID:g1041729
A/Note: the authors translated the codon GTC for residue 68 as Ile and AAC for residue
R/Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A/Reference number: H00822
A/Accession: G02131
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 25-397 <KAH>
A/Cross-references: EMBL:U36753; NID:g1208539; PID:AAA0957.1; PID:g1208540
C/Genetics:
A/Map position: 5q13
A/Intons: 28/1
C/Superfamily: ATP receptor P2u
F/1-36/Domain: activation peptide #status predicted <APT>
F/1-25/Domain: signal sequence #status predicted <SIG>
F/37-397/Product: proteinase-activated receptor 2 #status predicted <MAT>

Query Match 28.7% Score 114; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 4.1e-105;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 VGLPSNGMALWVLEFRTKKKHPAVIYMANLADLLSVIFPKIAVHIGNWYGEAL 147
DB 88 VGLPSNGMALWVLEFRTKKKHPAVIYMANLADLLSVIFPKIAVHIGNWYGEAL 147

QY 148 CNVLIGFFYGNMYCSILFMTCLSVORYWIVNPMGSHRKKANAIIGSLAIWLL 201
DB 148 CNVLIGFFYGNMYCSILFMTCLSVORYWIVNPMGSHRKKANAIIGSLAIWLL 201

RESULT 2
148705
proteinase activated receptor 2 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 148705
R/Nystedt, S.; Larsen, A.K.; Aberg, H.; Sundelin, J.
J. Biol. Chem. 270, 5950-5955, 1995
A/Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and
A/Reference number: 148705; MUID:95197620; PMID:7890726
A/Accession: 148705
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-399 <RBS>
A/Cross-references: UNIPROT:P55086; EMBL:Z48043; NID:g663020; PID:CAA88097.1; PID:g663
C/Superfamily: ATP receptor P2u

Query Match 8.6% Score 34; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.8e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 VLIQFFYGNMYCSILFMTCLSVORYWIVNPMGH 183
DB 152 VLIQFFYGNMYCSILFMTCLSVORYWIVNPMGH 185

RESULT 3
A37912
thrombin receptor precursor - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C/Accession: A37912
R/Vu, T.K.H.; Hung, D.T.; Wheaton, V.I.; Coughlin, S.R.
Cell 64, 1057-1068, 1991
A/Title: Molecular cloning of a functional thrombin receptor reveals a novel proteolytic
A/Reference number: A37912; MUID:91168254; PMID:1672265
A/Accession: A37912
A/Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: September 15, 2005, 09:14:06; Search time 169 Seconds

(without alignments)
1202.932 Million cell updates/sec

Title: US-10-643-627-63

Perfect score: 397

Sequence: 1 MRSPSAWLGLAAILLAAASL.....KHSRKSSSYSSSTTVKTSY 397

Scoring table:

GAPOP 60.0, Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size: 10

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 100 summaries

Database:

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 114 | 28.7 | 397 | 1 | PAR2_HUMAN |
| 2 | 37 | 9.3 | 397 | 1 | PAR2_RAT |
| 3 | 34 | 8.6 | 399 | 1 | PAR2_MOUSE |
| 4 | 34 | 8.6 | 399 | 1 | PAR2_MOUSE |
| 5 | 10 | 2.5 | 90 | 2 | Q16292 |
| 6 | 10 | 2.5 | 374 | 1 | PAR3_HUMAN |
| 7 | 10 | 2.5 | 376 | 2 | Q723W3 |
| 8 | 10 | 2.5 | 425 | 1 | PAR1_HUMAN |
| 9 | 10 | 2.5 | 425 | 1 | PAR1_PAPHA |
| 10 | 10 | 2.5 | 428 | 1 | PAR1_CRILLO |
| 11 | 10 | 2.5 | 430 | 1 | PAR1_MOUSE |
| 12 | 10 | 2.5 | 432 | 1 | PAR1_MOUSE |

ALIGNMENTS

RESULT 1
PAR2_HUMAN
ID: PAR2_HUMAN STANDARD; PRT; 397 AA.
AC: P55085; Q13317; Q13346;
DT: 01-OCT-1996 (Rel. 34, Created)
DT: 01-OCT-1996 (Rel. 34, Last sequence update)
DT: 25-OCT-2004 (Rel. 45, Last annotation update)
DE: Proteinase activated receptor 2 precursor (PAR-2) (thrombin receptor-like 1) (Coagulation factor II receptor-like 1).
GN: Name=PAR2; Synonyms=GERL1, PAR2;
OS: Homo sapiens (human).
OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;

RP [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=96048032; PubMed=7556175;
RT Nystedt S., Emilsson K., Larsson A.-K., Strombeck B., Sundelin J.;
RL "Molecular cloning and functional expression of the gene encoding the
human proteinase-activated receptor 2.";
RM Eur. J. Biochem. 232:84-89(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96177879; PubMed=8615752;
RA Boehm S.K., Kong W., Broemme D., Smeekens S.P., Anderson D.C.,
RA Connolly A.J., Kahn M.L., Nelken N.A., Coughlin S.R., Payan D.G.,
RA Bunnett N.W.;
RT "Molecular cloning, expression and potential functions of the human
proteinase-activated receptor-2.";
RL Biochem. J. 314:1009-1016(1996).
RN [3]
RP SEQUENCE OF 29-397 FROM N.A.
RX MEDLINE=96379236; PubMed=8784787;
RA Kahn M.L., Ishii K., Kuo W.L., Piper M., Connolly A.J., Shi Y.P.,
RA Mu R., Lin C.C., Coughlin S.R.;
RT "Conserved structure and adjacent location of the thrombin receptor
and protease-activated receptor 2 genes define a protease-activated
receptor gene cluster.";
RL Mol. Med. 2:349-357(1996).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS PHE-21; GLN-270 AND ALA-291.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Mickelson D.A.;
RT "SeattlesNP. NHLBI HL66682 program for genomic applications, UW-
FHCRG, Seattle, WA (URL: <http://pga.gs.washington.edu>)."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh P.,
RA Diatzenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedon T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunnarane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP -1- FUNCTION: Receptor for trypsin and trypsin-like enzymes coupled to
G proteins that stimulate phosphoinositide hydrolysis. May have a
role in the regulation of vascular tone.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed in tissues with especially
high levels in pancreas, liver, kidney, small intestine, and
colon. Moderate expression is detected in many organs, but none in
brain or skeletal muscle.
CC -1- PTM: A proteolytic cleavage generates a new amino terminus that
functions as a tethered ligand.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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OM protein - protein search, using sw model

Run on: September 15, 2005, 09:11:11 / Search time 167 Seconds
(without alignments)
919.424 Million cell updates/sec

Title: US-10-643-627-63

Perfect score: 397
Sequence: 1 MRSPSAWILGNALILAAAL.....KHSRKSSEYSSSTVTXTSY 397

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size: 10.

Total number of hits satisfying chosen parameters: 87

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database: A Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------------|--------|----|---------------------|
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| 2 | 296 | 74.6 | 397 | 2 | AAW01955 Human C14 |
| 3 | 296 | 74.6 | 397 | 2 | AAW51408 Human pro |
| 4 | 114 | 28.7 | 397 | 3 | AAW51408 Human pro |
| 5 | 114 | 28.7 | 397 | 5 | AAE26678 Human PAR |
| 6 | 114 | 28.7 | 397 | 5 | AAE26678 Human coa |
| 7 | 114 | 28.7 | 397 | 7 | ABG73508 Human par |
| 8 | 114 | 28.7 | 397 | 7 | ADBE62812 Human pro |
| 9 | 114 | 28.7 | 397 | 8 | AD6161221 Human coa |
| 10 | 114 | 28.7 | 397 | 8 | AD029311 Human GPC |
| 11 | 114 | 28.7 | 397 | 8 | AD674020 Human G-P |
| 12 | 114 | 28.7 | 398 | 2 | AAR66921 Human C14 |
| 13 | 114 | 28.7 | 398 | 2 | AAW01953 Human C14 |
| 14 | 114 | 28.7 | 398 | 2 | AD128655 Human mod |
| 15 | 91 | 22.9 | 341 | 8 | AD128654 Human mod |
| 16 | 91 | 22.9 | 355 | 8 | AD128653 Human mod |
| 17 | 91 | 22.9 | 397 | 6 | ABP81907 Human pro |
| 18 | 91 | 22.9 | 397 | 7 | ADK52594 Hematolog |
| 19 | 91 | 22.9 | 397 | 7 | ADN39997 Cancer/an |
| 20 | 91 | 22.9 | 397 | 8 | ADR46675 Cancer-as |
| 21 | 57 | 14.4 | 389 | 8 | AD028601 Human PAR |
| 22 | 39 | 9.8 | 54 | 8 | AD128666 Human pro |
| 23 | 37 | 9.3 | 397 | 7 | AD662810 Rat Prote |
| 24 | 34 | 8.6 | 395 | 2 | AAR66920 Murine C1 |
| 25 | 34 | 8.6 | 399 | 2 | AAW01952 Murine C1 |
| | | | | | AAR66922 Murine C1 |

ALIGNMENTS

| | | | | | | |
|----|----|-----|-----|---|-----------|---------------------|
| 26 | 34 | 8.6 | 399 | 2 | AAW01954 | AAW01954 Murine C1 |
| 27 | 34 | 8.6 | 399 | 7 | ABR63562 | ABr63562 Delayed h |
| 28 | 34 | 8.6 | 399 | 7 | AD029312 | AD029312 Mouse GPC |
| 29 | 33 | 8.3 | 58 | 5 | ABU67239 | ABU67239 G-protein |
| 30 | 33 | 8.3 | 58 | 6 | ABP54020 | ABP54020 Human pro |
| 31 | 33 | 8.3 | 58 | 8 | AD028760 | AD028760 Human pro |
| 32 | 33 | 8.3 | 58 | 8 | AD005264 | AD005264 Proteinas |
| 33 | 33 | 6.3 | 25 | 3 | AAV45037 | AAV45037 Human pro |
| 34 | 21 | 5.3 | 21 | 5 | AAU10420 | AAU10420 PAR2 pepd |
| 35 | 20 | 5.0 | 20 | 6 | ABP82705 | ABP82705 G protein |
| 36 | 20 | 5.0 | 21 | 5 | AAU10421 | AAU10421 PAR2 pepd |
| 37 | 18 | 4.5 | 18 | 6 | ABP82706 | ABP82706 G protein |
| 38 | 18 | 4.5 | 18 | 6 | ABP82707 | ABP82707 G protein |
| 39 | 15 | 3.8 | 68 | 5 | ADK35286 | ADK35286 Novel hum |
| 40 | 14 | 3.5 | 16 | 6 | ABP82708 | ABP82708 G protein |
| 41 | 14 | 3.5 | 20 | 3 | AAW35651 | AAW35651 Human PAR |
| 42 | 12 | 3.0 | 12 | 2 | AAW76406 | AAW76406 Human PAR |
| 43 | 11 | 2.8 | 20 | 3 | AAW35652 | AAW35652 Mouse PAR |
| 44 | 10 | 2.5 | 13 | 2 | AAR66890 | AAR66890 Agonist p |
| 45 | 10 | 2.5 | 13 | 2 | AAW01923 | AAW01923 C140 rece |
| 46 | 10 | 2.5 | 15 | 5 | ABG35288 | ABG35288 Human PAR |
| 47 | 10 | 2.5 | 15 | 5 | ABG35286 | ABG35286 Human PAR |
| 48 | 10 | 2.5 | 15 | 5 | ABG35287 | ABG35287 Human PAR |
| 49 | 10 | 2.5 | 15 | 5 | ABG35289 | ABG35289 Human PAR |
| 50 | 10 | 2.5 | 15 | 5 | ABG35285 | ABG35285 Human PAR |
| 51 | 10 | 2.5 | 26 | 2 | AAR27238 | AAR27238 Thrombin |
| 52 | 10 | 2.5 | 319 | 4 | AAW82760 | AAW82760 Rat G-pro |
| 53 | 10 | 2.5 | 319 | 4 | AD029401 | AD029401 Mouse GPC |
| 54 | 10 | 2.5 | 371 | 5 | ABG35299 | ABG35299 Human PAR |
| 55 | 10 | 2.5 | 374 | 2 | AAW51406 | AAW51406 Human pro |
| 56 | 10 | 2.5 | 374 | 6 | ABG73509 | ABG73509 Human par |
| 57 | 10 | 2.5 | 374 | 6 | ABP81908 | ABP81908 Human pro |
| 58 | 10 | 2.5 | 374 | 7 | ADBE67661 | ADBE67661 Human PAR |
| 59 | 10 | 2.5 | 374 | 8 | AD029313 | AD029313 Human GPC |
| 60 | 10 | 2.5 | 374 | 8 | ADQ97469 | ADQ97469 Human can |
| 61 | 10 | 2.5 | 374 | 8 | ADQ39889 | ADQ39889 Human myo |
| 62 | 10 | 2.5 | 374 | 8 | ADQ32990 | ADQ32990 Proteinas |
| 63 | 10 | 2.5 | 402 | 5 | ABG35298 | ABG35298 Human PAR |
| 64 | 10 | 2.5 | 425 | 2 | AAR27240 | AAR27240 Human thr |
| 65 | 10 | 2.5 | 425 | 2 | AAW60698 | AAW60698 Fragment |
| 66 | 10 | 2.5 | 425 | 2 | AAW51407 | AAW51407 Human pro |
| 67 | 10 | 2.5 | 425 | 2 | AAV49570 | AAV49570 Human thr |
| 68 | 10 | 2.5 | 425 | 5 | AAE17032 | AAE17032 Human thr |
| 69 | 10 | 2.5 | 425 | 5 | ABG35300 | ABG35300 Human PAR |
| 70 | 10 | 2.5 | 425 | 5 | AAW80697 | AAW80697 Human thr |
| 71 | 10 | 2.5 | 425 | 6 | ABG73511 | ABG73511 Human thr |
| 72 | 10 | 2.5 | 425 | 6 | ABR47449 | ABR47449 Breast ca |
| 73 | 10 | 2.5 | 425 | 6 | ABP81919 | ABP81919 Human thr |
| 74 | 10 | 2.5 | 425 | 7 | ADBE8075 | ADBE8075 Human pro |
| 75 | 10 | 2.5 | 425 | 7 | ADG89876 | ADG89876 Human pro |
| 76 | 10 | 2.5 | 425 | 7 | ADG89876 | ADG89876 Human coa |
| 77 | 10 | 2.5 | 425 | 8 | ADL14208 | ADL14208 Novel hum |
| 78 | 10 | 2.5 | 425 | 8 | ADN04016 | ADN04016 Antipsoi |
| 79 | 10 | 2.5 | 425 | 8 | ADQ29309 | ADQ29309 Human GPC |
| 80 | 10 | 2.5 | 425 | 8 | AD018985 | AD018985 Human bof |
| 81 | 10 | 2.5 | 425 | 8 | ADR45608 | ADR45608 Human G-P |
| 82 | 10 | 2.5 | 425 | 8 | ADSB4489 | ADSB4489 Human pro |
| 83 | 10 | 2.5 | 426 | 3 | AAV45035 | AAV45035 Human thr |
| 84 | 10 | 2.5 | 430 | 8 | AD029310 | AD029310 Mouse GPC |
| 85 | 10 | 2.5 | 432 | 7 | ADBE8073 | ADBE8073 Rat Prote |
| 86 | 10 | 2.5 | 432 | 7 | ADBE8069 | ADBE8069 Rat Prote |
| 87 | 10 | 2.5 | 892 | 2 | AAW16314 | AAW16314 Human thr |

RESULT 1
AAR66923 standard; protein; 397 AA.
XX AAR66923;
XX AC
XX